

FIG. 1A

| | | |
|---|---------------------------|-----|
| 10 | 30 | 50 |
| GAATT CGG CAC GAG CTG AGGGT GAG CC AAG CC TGC CAT GTAG TGC AC GCA GG AC AT CA | | |
| 70 | 90 | 110 |
| ACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCAA | | |
| 130 | 150 | 170 |
| CCTTCAAAGTTCAAGTAGTGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCCCTAC | | |
| | M D D S T E R E Q S R L T | |
| 190 | 210 | 230 |
| TTCTTGCCTTAAGAAAAGAGAAGAAAATGAAACTGAAGGAGTGTGTTCCATCCTCCCACG | | |
| S C L K K R E E M K L K E C V S I L P R | | |
| 250 | 270 | 290 |
| GAAGGAAAGCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCT | | |
| K E S P S V R S S K D G K <u>L L A A T L L</u> | | |
| 310 | 330 | 350 |
| GCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTCTACCAAGGTGGCCGCCCTGCA | | |
| <u>L A L L S C C L T V V S F Y Q V A A L</u> Q | | |
| 370 | 390 | 410 |
| AGGGGACCTGGCCAGCCTCCGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGC | | |
| G D L A S L R A E L Q G H H A E K L P A | | |
| 430 | 450 | 470 |
| AGGAGCAGGAGCCCCAAGGCCGCTGGAGGAAGCTCCAGCTGTCAACCGCGGGACTGAA | | |
| G A G A P K A G L E E A P A V T A G L K | | |
| 490 | 510 | 530 |
| AATCTTGAAACCACCAAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG | | |
| I F E P P A P G E G N S S Q N S R N K R | | |
| 550 | 570 | 590 |
| TGCCGTTCAAGGTCCAGAAGAACAGTCACTCAAGACTGCTGCAACTGATTGCAGACAG | | |
| A V Q G P E E T V T Q D C L Q L I A D S | | |

FIG. 1B

610 630 650
 TGAAACACCAACTATAACAAAAAGGATCTTACACATTGTTCCATGGCTTCAGCTTAA
 E T P T I Q K G S Y T F V P W L L S F K
 670 690 710
 AAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTT
 R G S A L E E K E N K I L V K E T G Y F
 730 750 770
 TTTTATATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCA
 F I Y G Q V L Y T D K T Y A M G H L I Q
 790 810 830
 GAGGAAGAAGGTCCATGTCTTGGGGATGAATTGAGTCTGGTACTTGGTTCGATGTAT
 R K K V H V F G D E L S L V T L F R C I
 850 870 890
 TCAAAATATGCCTGAAACACTACCCAATAATTCCCTGCTATTAGCTGGCATTGCAAAACT
 Q N M P E T L P N N S C Y S A G I A K L
 910 930 950
 GGAAGAAGGAGATGAACCTCAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGA
 E E G D E L Q L A I P R E N A Q I S L D
 970 990 1010
 TGGAGATGTCACATTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCAGTCTGT
 G D V T F F G A L K L L
 1030 1050 1070
 AGCTATTTCCCTTCTCTGTACCTCTAAGAAGAAAGAATCTAAGTGGAAATACCAAA
 1090 1110 1130
 AAAAAAAAAAAAAAAAAAAAAAGTAGTTAAAAAAAAAAAAAA
 1150 1170
 AAAAAAAAAAAAAAAACTCGGAGGGGG

FIG. 2A

| | | |
|--|-----|-------|
| 10 | 30 | 50 |
| GAATTGGCACGAGCTCAAAGGCCTAGACCTCAAAGTGCTCCTCGTGGATGGATGAG | | |
| | | M D E |
| | | |
| 70 | 90 | 110 |
| TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTGCTCCGAGAAAGGAGAAGATATG | | |
| S A K T L P P P C L C F C S E K G E D M | | |
| 130 | 150 | 170 |
| AAAGTGGATATGATCCCATCACTCCGCAGAAGGAGGAGGGTGCCTGGTTGGATCTGC | | |
| K V G Y D P I T P Q K E E G A W F G I C | | |
| 190 | 210 | 230 |
| AGGGATGGAAGGCTGGCTGCTACCCCTCCTGCTGGCCCTGTTGCCAGCAGTTACACA | | |
| R D G R <u>L L A A T L L L A L L S S S F T</u> | | |
| 250 | 270 | 290 |
| GCGATGTCCTTGTACCAGTTGGCTGCCTTGCAAGCAGACCTGATGAACCTGCGCATGGAG | | |
| <u>A M S L Y O L A A L Q A D L M N L R M E</u> | | |
| 310 | 330 | 350 |
| CTGCAGAGCTACCGAGGTTCAAGAACACCAGCCGCCGCGGGTGCTCCAGAGTTGACCGCT | | |
| L Q S Y R G S A T P A A A G A P E L T A | | |
| 370 | 390 | 410 |
| GGAGTCAAACTCCTGACACCGGGCAGCTCCTCGACCCCCACAACCTCCAGCCGGGCCACAGG | | |
| G V K L L T P A A P R P H N S S R G H R | | |
| 430 | 450 | 470 |
| AACAGACGCGTTCCAGGGACCAGAGGAAACAGAACAGATGTAGACCTCTCAGCTCCT | | |
| N R R A F Q G P E E T E Q D V D L S A P | | |
| 490 | 510 | 530 |
| CCTGCACCATGCCTGCCTGGATGCCGCATTCTAACATGATGATAATGGAATGAACCTC | | |
| P A P C L P G C R H S Q H D D N G M N L | | |
| 550 | 570 | 590 |
| AGAAACATCATTCAAGACTGTCAGCTGATTGCAGACAGCGACAGCCGACTATACGA | | |
| R N I I Q D C L Q L I A D S D T P T I R | | |

FIG. 2B

610 630 650

AAAGGAAC TTACACATTGTTCCATGGCTTCTCAGCTTAAAAGAGGAAATGCCTGGAG
K G T Y T F V P W L L S F K R G N A L E
670 690 710

GAGAAAGAGAACAAAATAGTGGTGAGGCAAACAGGCTATTCTTCATCTACAGCCAGGTT
E K E N K I V V R Q T G Y F F I Y S Q V
730 750 770

CTATACACGGACCCCATCTTGCTATGGGTATGTCATCCAGAGGAAGAAAGTACACGTC
L Y T D P I F A M G H V I Q R K K V H V
790 810 830

TTTGGGGACGAGCTGAGCCTGGTGACCCCTGGTCCGATGTATTCAAATATGCCAAAACA
F G D E L S L V T L F R C I Q N M P K T
850 870 890

CTGCCAACAAATTCCCTGCTACTCGGCTGGCATCGCGAGGCTGGAAGAAGGAGATGAGATT
L P **N** N S C Y S A G I A R L E E G D E I
910 930 950

CAGCTTGCAATTCCCTGGGAGAATGCACAGATTTCACGCAACGGAGACGACACCTCTTT
Q L A I P R E N A Q I S R N G D D T F F
970 990 1010

GGTGCCCTAAAAC TGCTGTAAC TCACTTGCTGGAGTGCGTGATCCCCTCCCTCGTCTTC
G A L K L L
1030 1050 1070

TCTGTACCTCCGAGGGAGAACAGACGACTGGAAAAACTAAAAGATGGGAAAGCCGTCA
1090 1110 1130

GCGAAAGTTTCTCGTGACCCGTTGAATCTGATCCAAACCAGGAAATATAACAGACAGCC
1150 1170 1190

FIG. 3A

| | | 1 | 50 | 100 | 150 | 200 |
|-------|---------------------------------|--|---|-----------------------------------|-----------------------------------|-----|
| Hagp3 | MDDSTER.EQ | SRLTSCLIKRR | EEMKLKECVS | ILPRKESPSV | RSSKD G LLA | |
| Magp3 | MDESAKTLPP | PCLCFCS EKG | EDMKVGYDPI | TPQKEEGAWF | GICRD G RL LLA | |
| cons | MD.S... . . . | L.C.K. | E.MK. | E. | DG.LLA | |
| | | | | | | |
| | | 51 | | | | |
| Hagp3 | <u>ATLL</u> <u>LL</u> <u>SC</u> | <u>CLTVV</u> <u>SFY</u> <u>YV</u> | <u>AALQ</u> <u>GDI</u> <u>ASL</u> | <u>RAELQ</u> <u>GHHAE</u> | <u>KLPAGAG</u> <u>A</u> <u>PK</u> | |
| Magp3 | <u>ATLL</u> <u>LL</u> <u>SS</u> | <u>SFT</u> <u>AMS</u> <u>LYQ</u> <u>OL</u> | <u>AALQ</u> <u>ADL</u> <u>MN</u> <u>L</u> | <u>RMELQ</u> <u>SYR</u> <u>GS</u> | <u>ATPAA</u> <u>AGA</u> <u>PE</u> | |
| cons | ATLLLALLS. | ..T..S.YQ. | AALQ.DL..L | R.ELQ.. . . | PA.AGAP. | |
| | | | | | | |
| | | 101 | | | | |
| Hagp3 | AGLEEA PAVT | AGLKIFEP PA | PCEGNSSQNS | RNKRAVQGPE | ET. | |
| Magp3 |LT | AGVKLL ITPAA | PRPHNSR GH | NRRAFQGPE | ETEQD V DLSA | |
| cons |T | AG.K...P.A | P...NSS... . | RN.RA.QGPE | ET. | |
| | | | | | | |
| | | 151 | | | | |
| Hagp3 | | | | | | |
| Magp3 | PPAPCLPGCR | HSQHDDNGMN | LRNIIQDC LO | LIADSD T PTI | RKGTYTFV VPW | |
| cons | | | | | | |

FIG. 3B

FIG. 4A

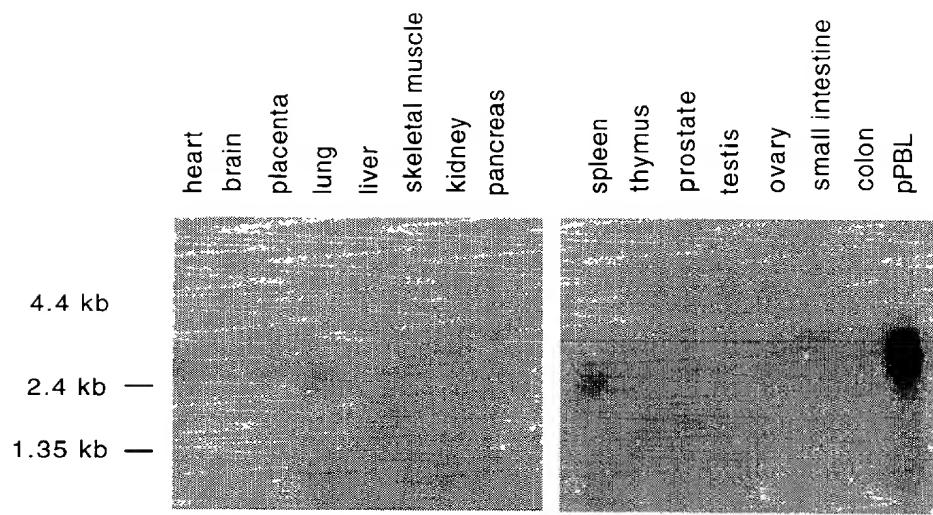


FIG. 4B

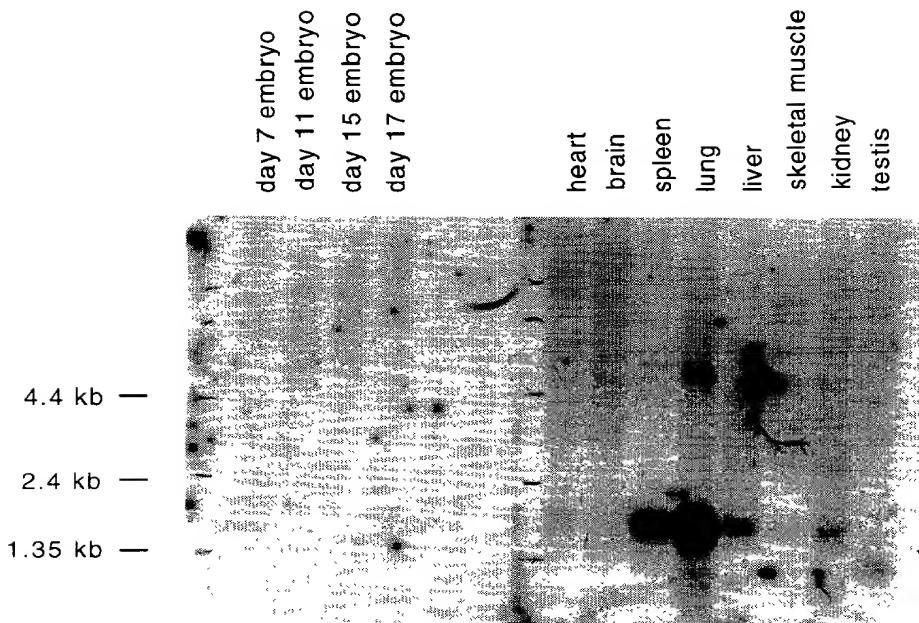


FIG. 5A



FIG. 5B

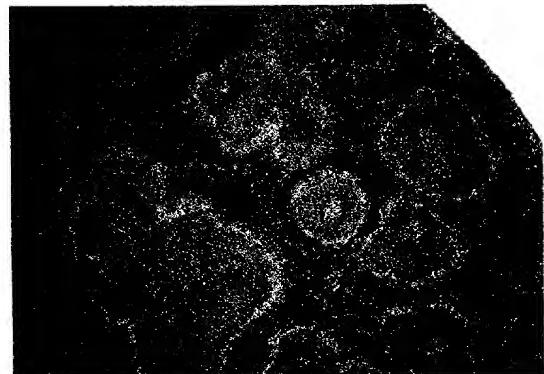


FIG. 5C

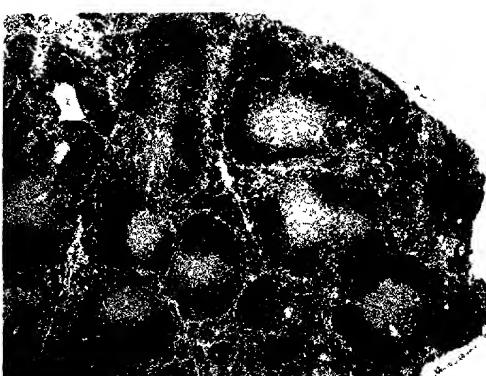


FIG. 5D

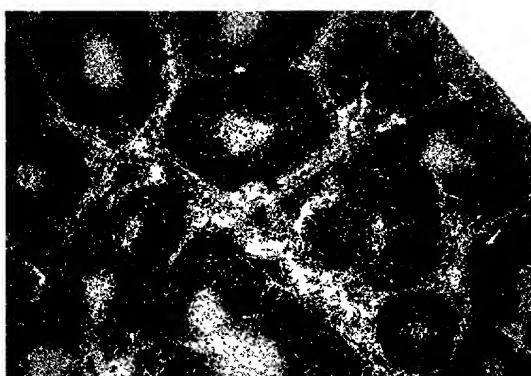


FIG. 5E

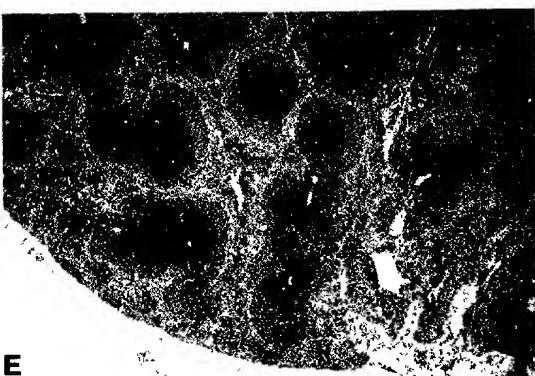


FIG. 5F

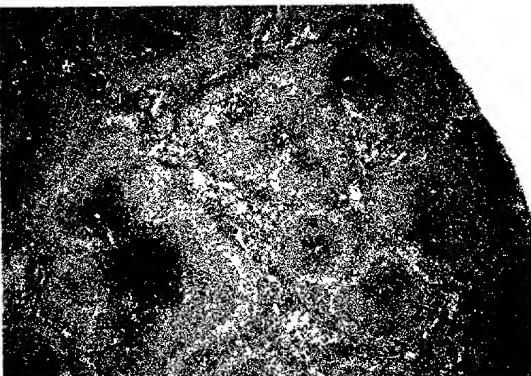


FIG. 6A

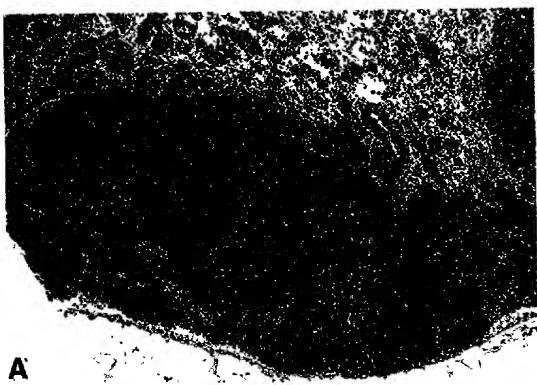


FIG. 6B

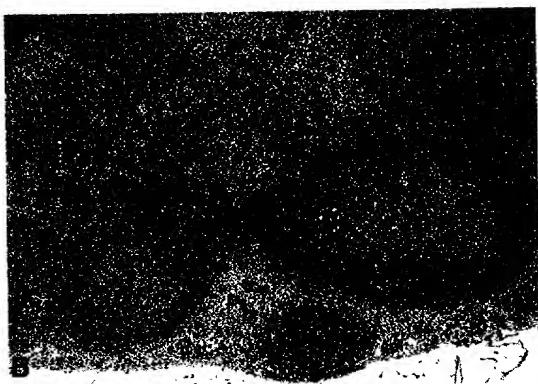


FIG. 6C



FIG. 6D

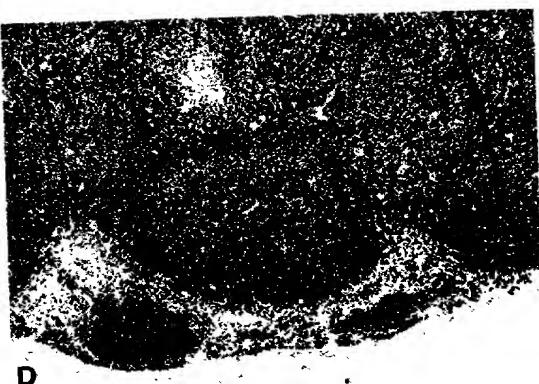


FIG. 6E



FIG. 6F

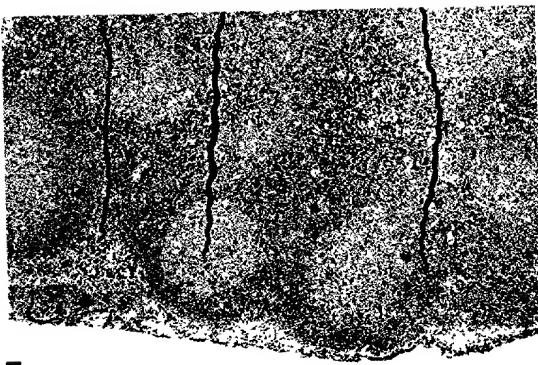
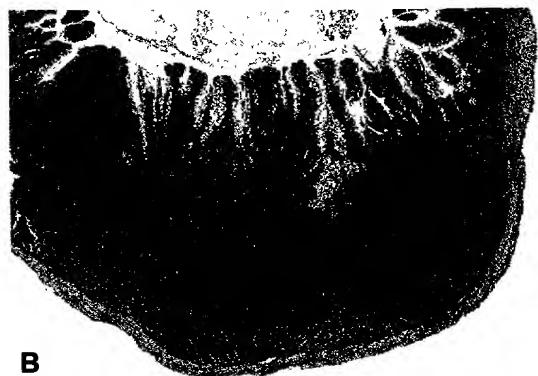


FIG. 7A



A

FIG. 7B



B

FIG. 7C



C

FIG. 7D



D

FIG. 7E



E

FIG. 7F



F

FIG. 8A

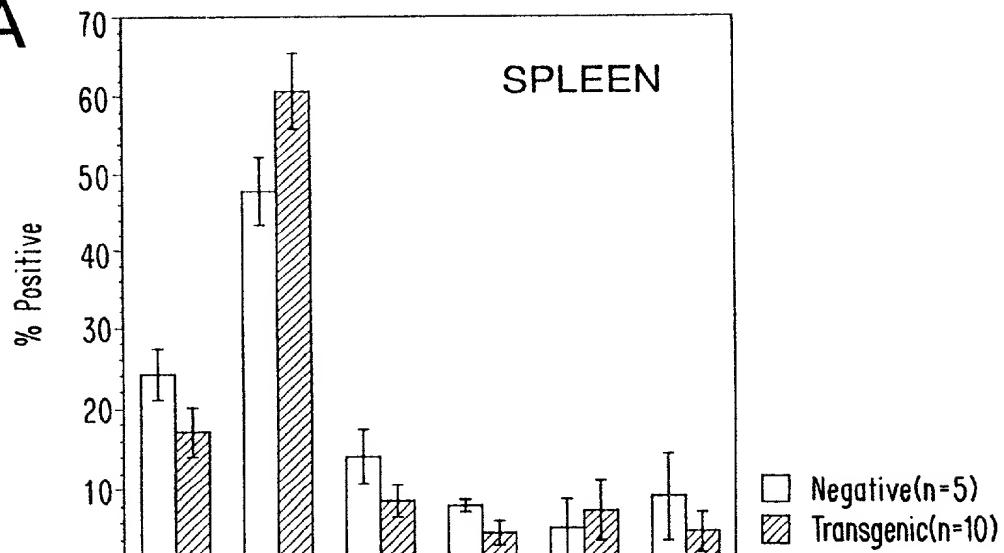


FIG. 8B

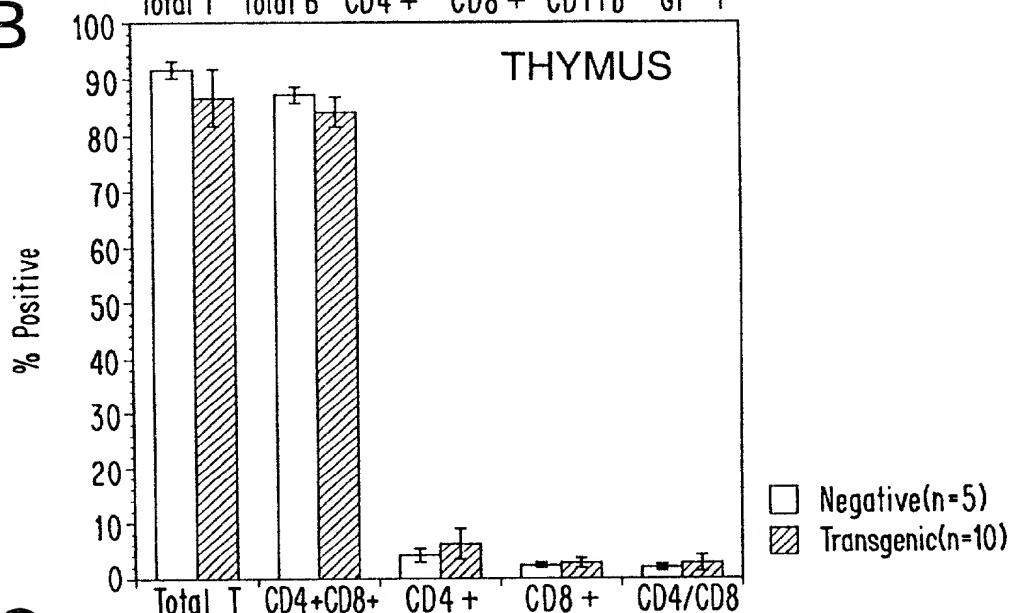


FIG. 8C

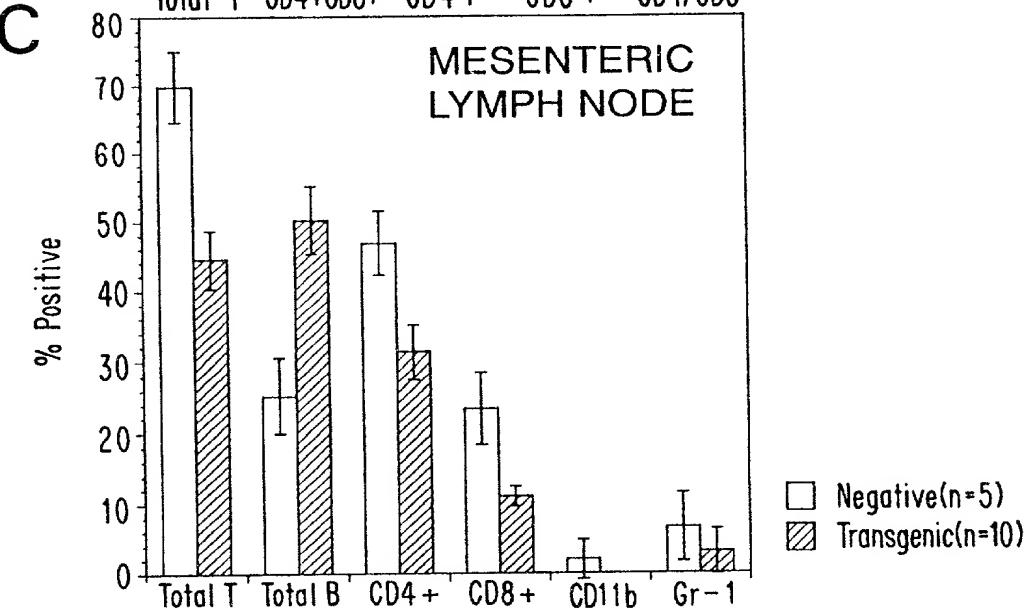


FIG. 9A

FIG. 9B

| E | <u>E/F loop</u> | F | G | H | <u>H/I loop</u> | |
|----------------|--------------------------|----------|--|---------------|---------------------|-------------|
| -H-V----V----- | -Y P----- | -T-----C | -W-----S-----F----- | -S-----F----- | -T-----T-----T----- | Consensus |
| SHKVYMRNS----- | KYPODLVMMEEGRMMMSYC----- | ----- | TTGQWARSYYLGAVENLTSAHDLYVNVSELSLYNFEESQ----- | ----- | ----- | Human FasL |
| 208- | ----- | ----- | TTGQWARSYYLGAVENLTSAHDLYVNVSELSLYNFEESQ----- | ----- | -281 | Human FasL |
| 206- | ----- | ----- | TTGQIWAHSSYYLGAVENLTSAHDLYVNVSELSLYNFEESQ----- | ----- | -279 | Mouse FasL |
| 205- | ----- | ----- | TTGQIWAHSSYYLGAVENLTSAHDLYVNVSELSLYNFEESQ----- | ----- | -278 | Rat FasL |
| 190- | ----- | ----- | ----- | ----- | -261 | Human CD40L |
| 189- | ----- | ----- | ----- | ----- | -260 | Mouse CD40L |
| 212- | ----- | ----- | ----- | ----- | -285 | Human AGP3 |
| 236- | ----- | ----- | ----- | ----- | -309 | Mouse AGP3 |
| 234- | ----- | ----- | ----- | ----- | -316 | Mouse OPGL |
| 235- | ----- | ----- | ----- | ----- | -317 | Human OPGL |
| 201- | ----- | ----- | ----- | ----- | -281 | Human TRAIL |
| 210- | ----- | ----- | ----- | ----- | -291 | Mouse TRAIL |
| 159- | ----- | ----- | ----- | ----- | -234 | Human CD30L |
| 164- | ----- | ----- | ----- | ----- | -239 | Mouse CD30L |
| 158- | ----- | ----- | ----- | ----- | -244 | Human Lytβ |
| 223- | ----- | ----- | ----- | ----- | -306 | Mouse Lytβ |
| 132- | ----- | ----- | ----- | ----- | -205 | Human TNFβ |
| 129- | ----- | ----- | ----- | ----- | -202 | Mouse TNFβ |
| 153- | ----- | ----- | ----- | ----- | -233 | Human TNFα |
| 155- | ----- | ----- | ----- | ----- | -235 | Mouse TNFα |

FIG. 10A FIG. 10D FIG. 10G

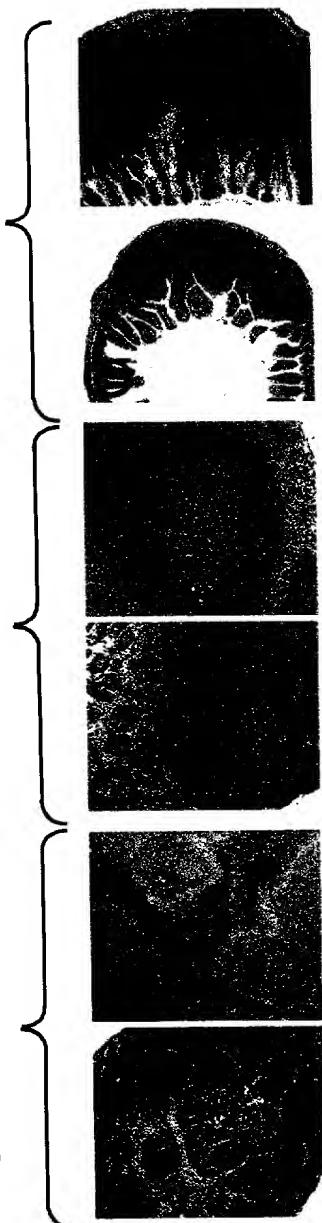


FIG. 10B FIG. 10E FIG. 10H

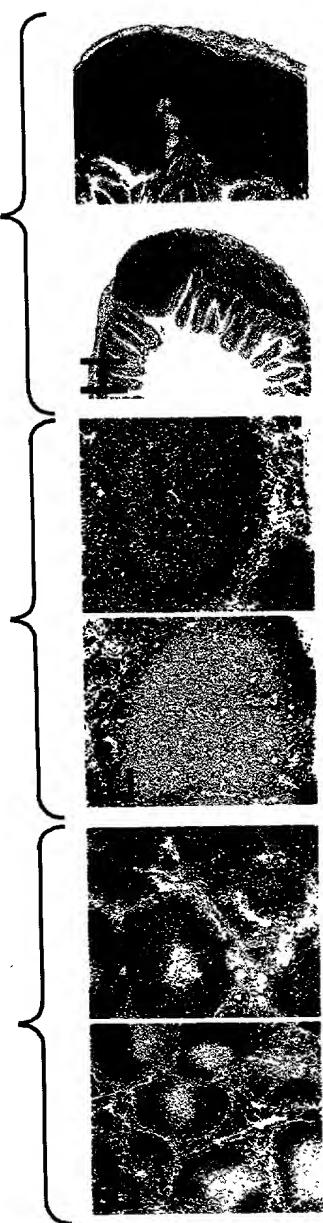


FIG. 10C FIG. 10F FIG. 10I

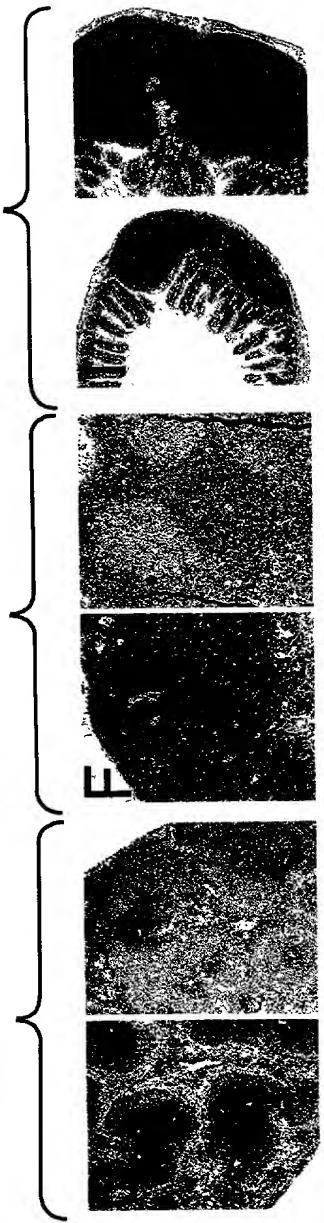


FIG. 11A

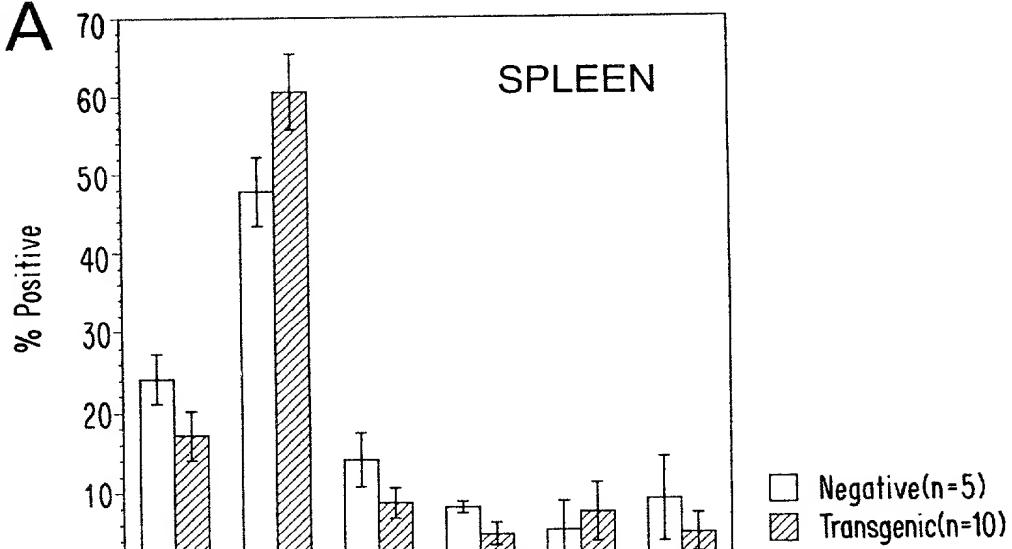


FIG. 11B

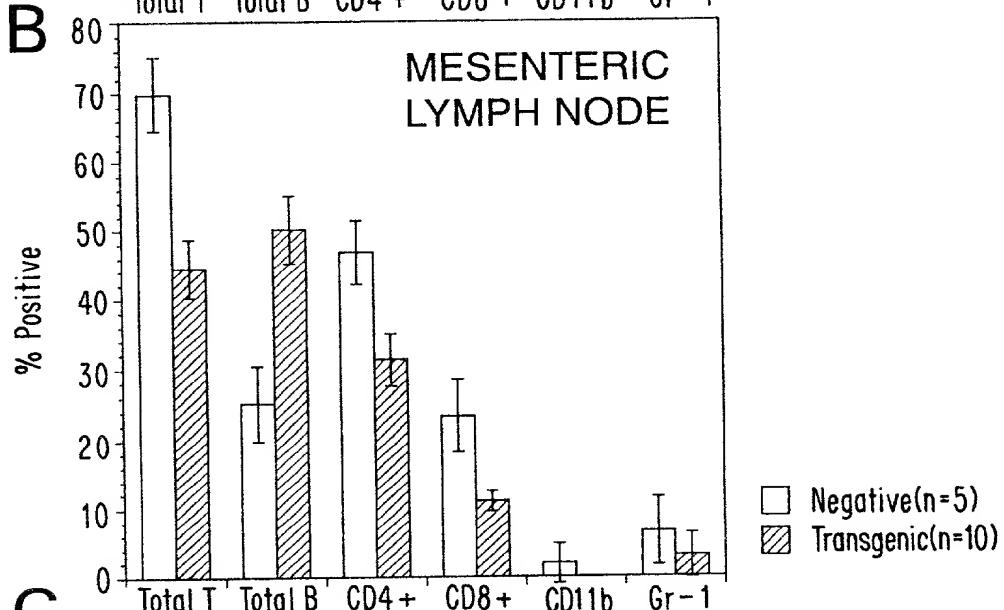


FIG. 11C

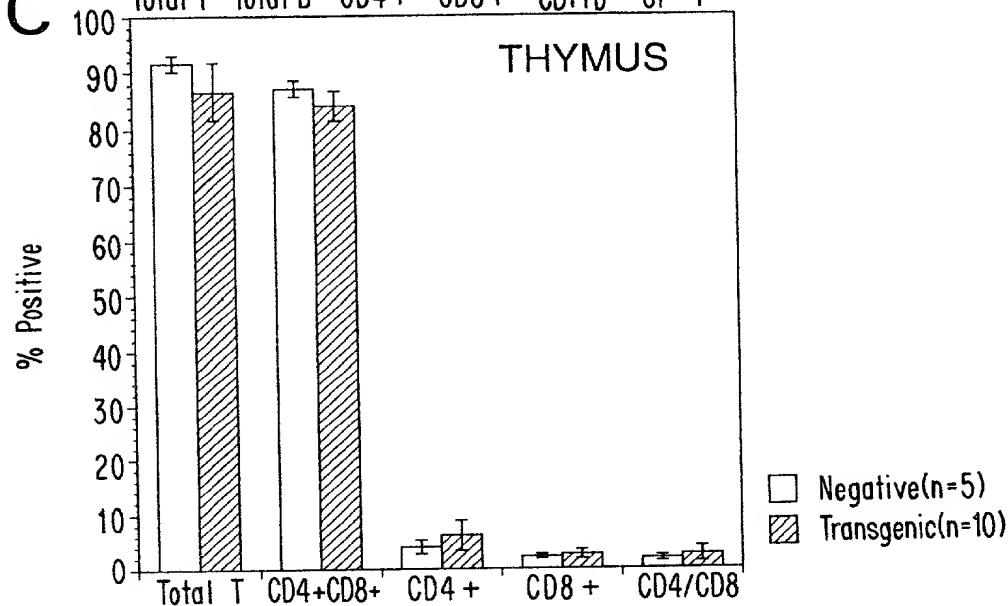


FIG. 12A

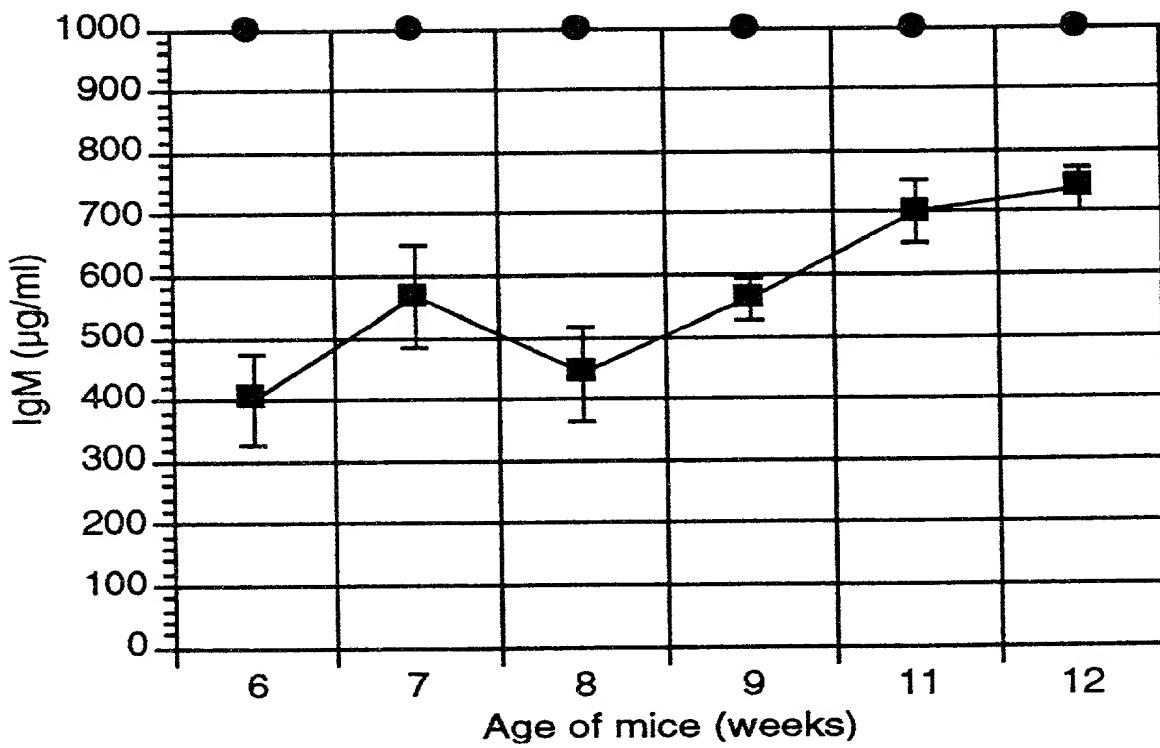


FIG. 12B

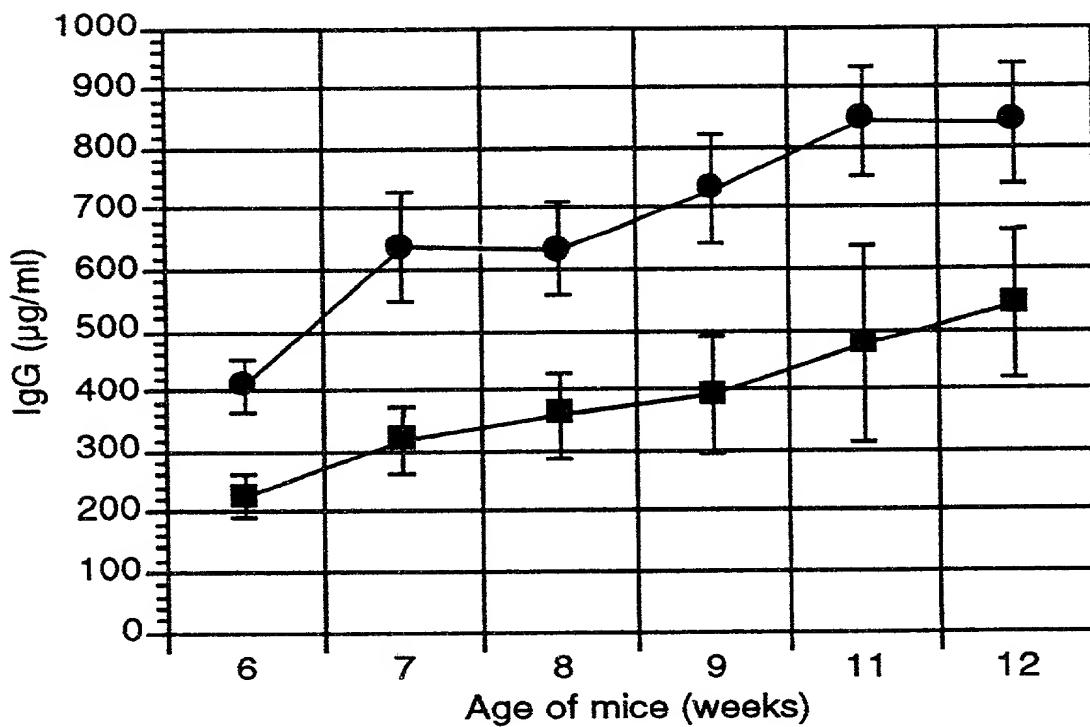


FIG. 12C

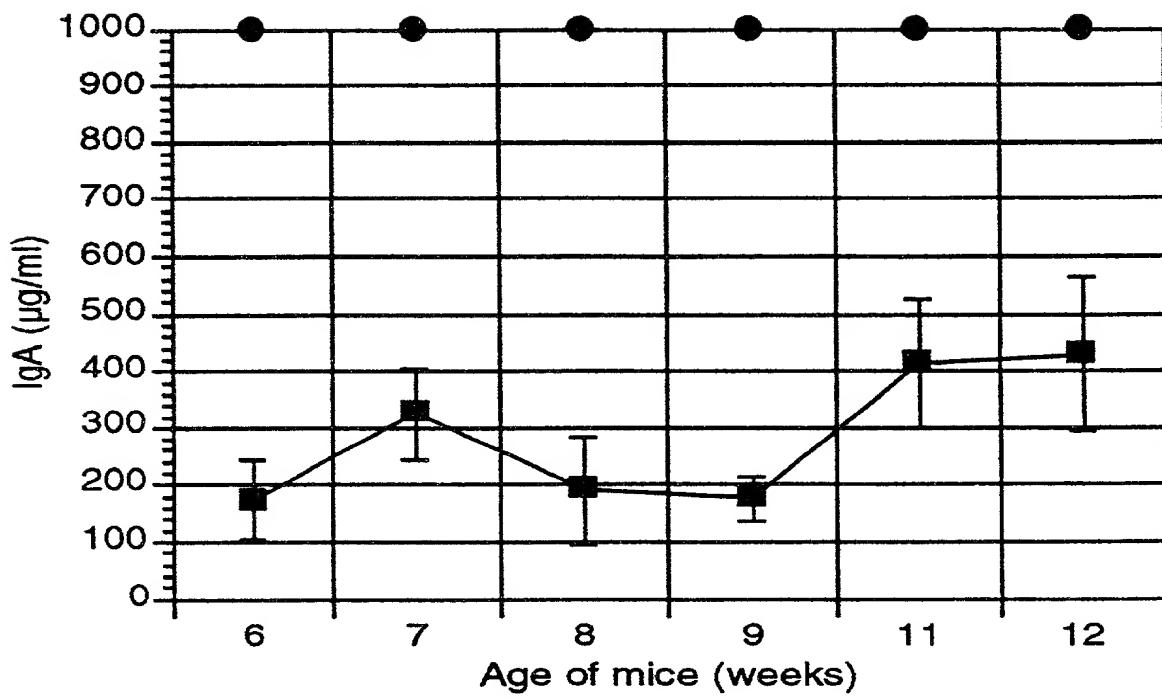


FIG. 12D

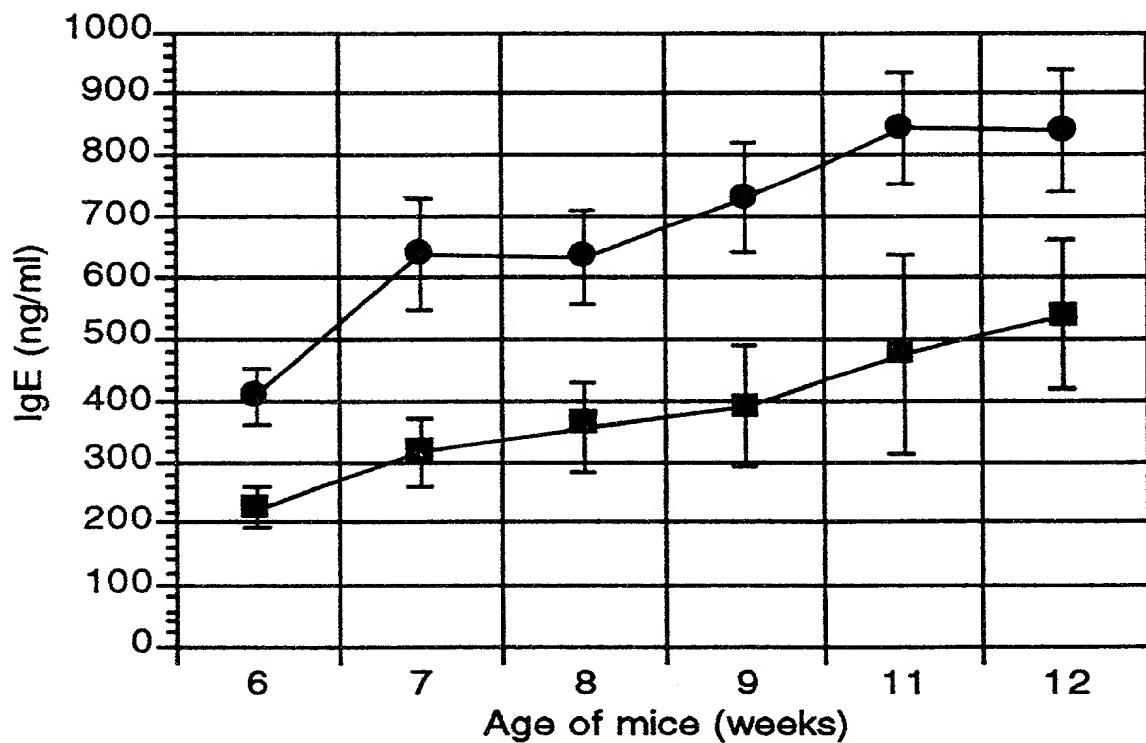


FIG. 13A

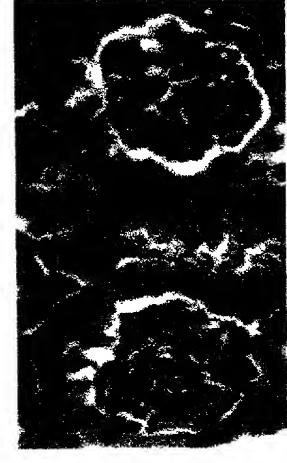


FIG. 13D

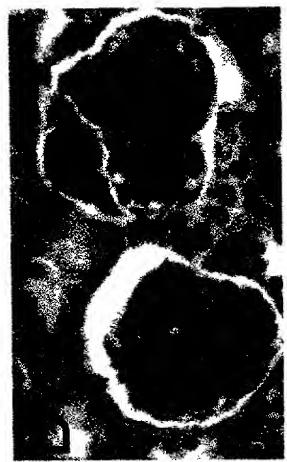


FIG. 13G



FIG. 13B

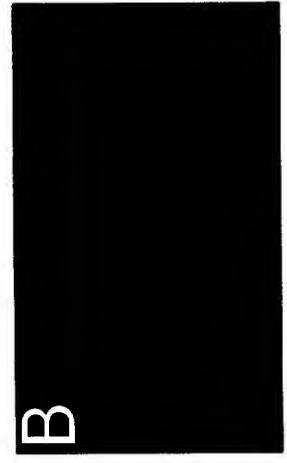


FIG. 13E

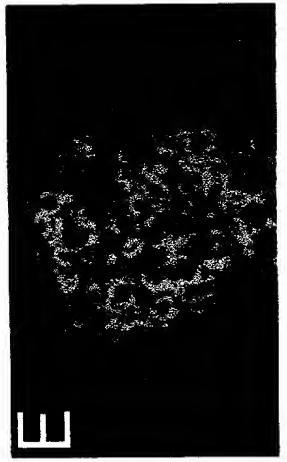


FIG. 13H

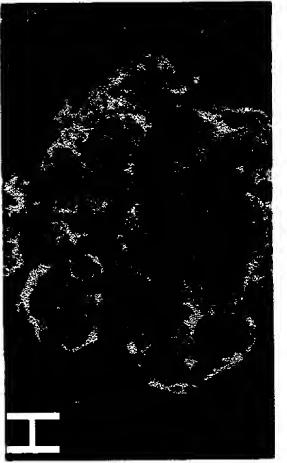


FIG. 13C

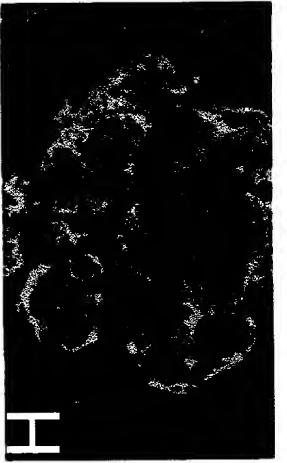


FIG. 13F

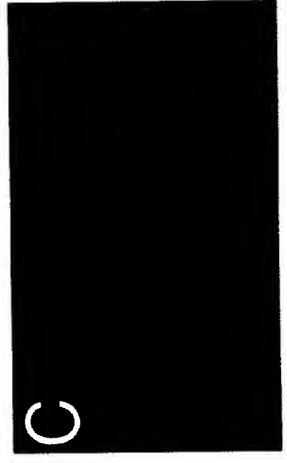
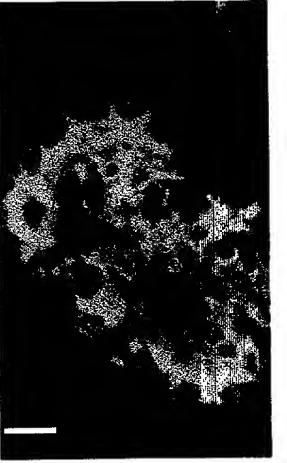


FIG. 13I



F

C

FIG. 14A

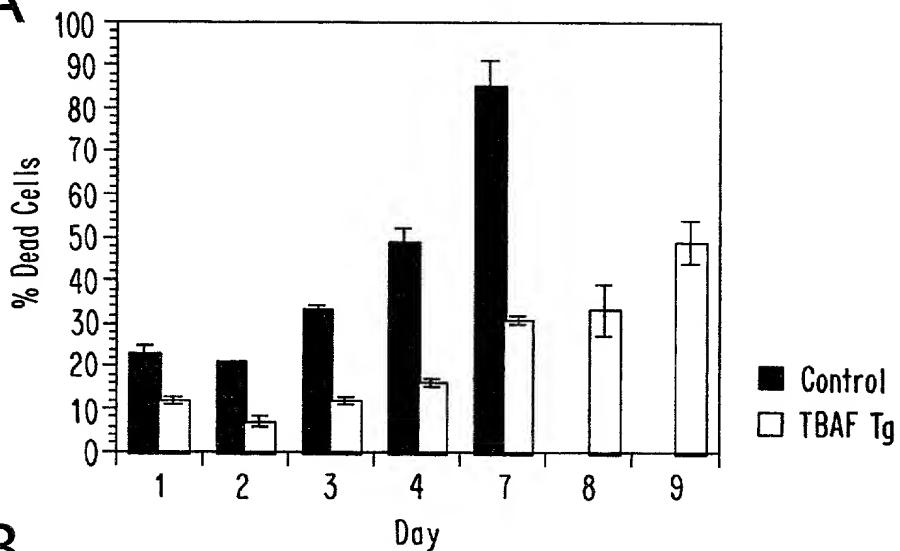


FIG. 14B

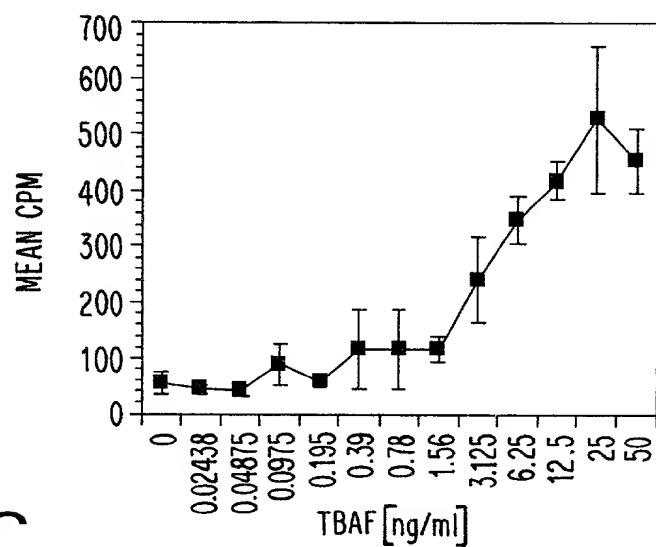


FIG. 14C

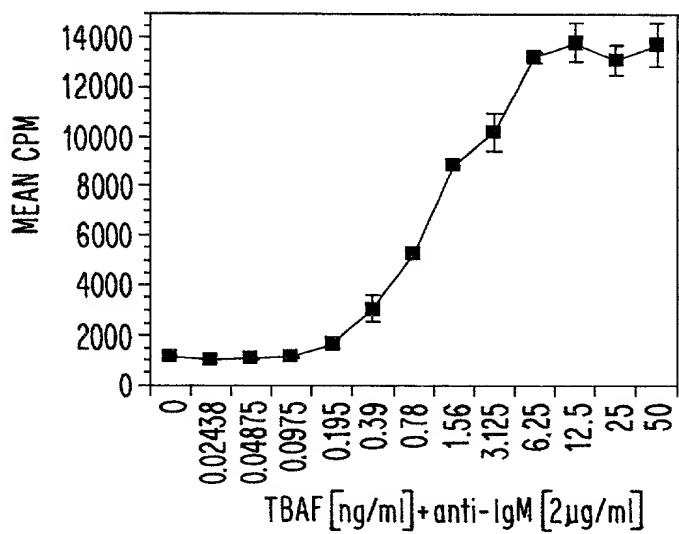


FIG. 15

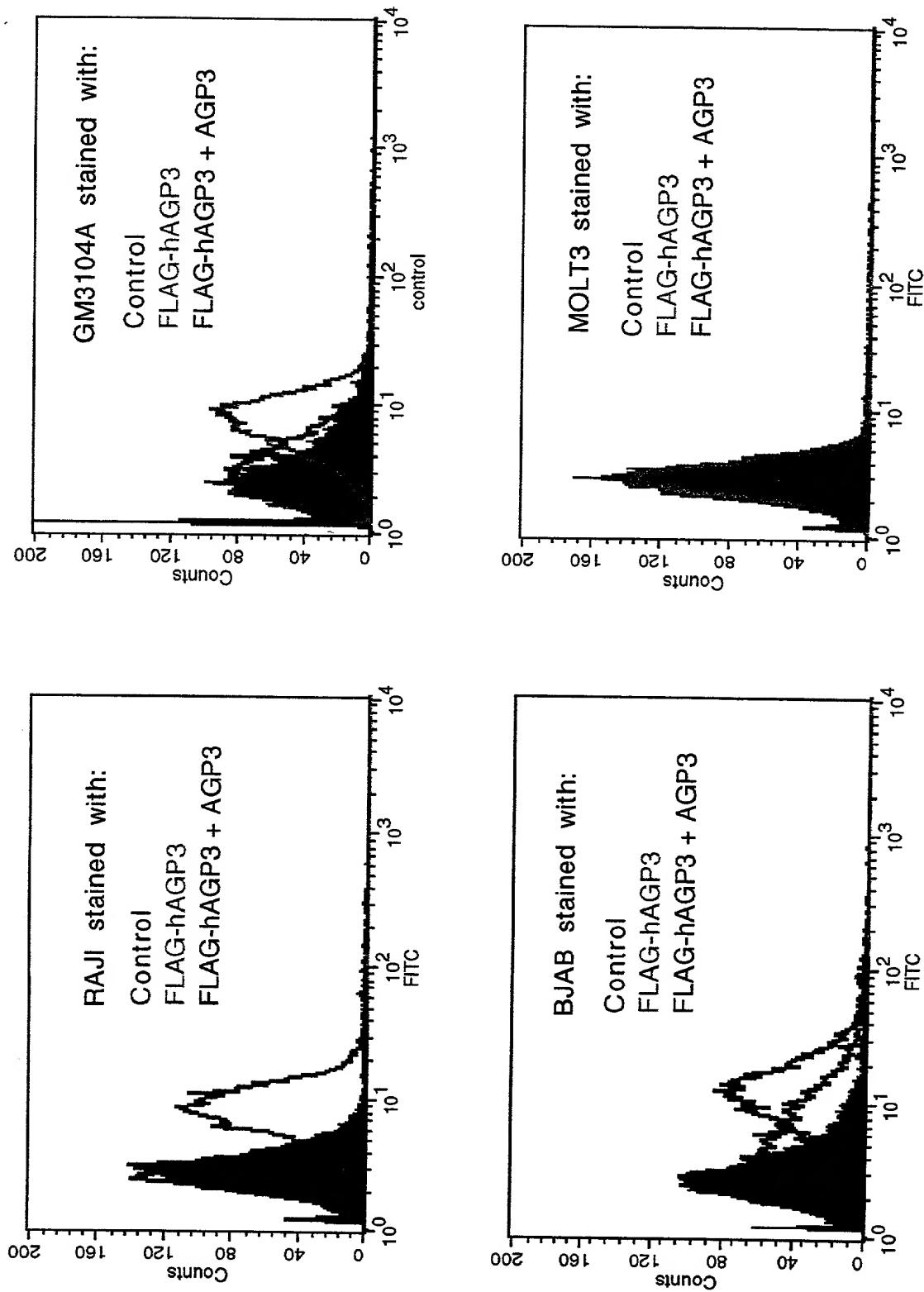


FIG. 16

Alignment of AGP3-binding pools 13B4 and 13H11
N-terminal sequence

1 GTCGACCCACGCGTCCG ATCCTGAGTAATGAGTGGCCTGGCC 43
1 GTCGACCCACGCGTCCGAATAAGCATCCTGAGTAATGAGTGGCCTGGCC 50
44 GGAGCAGGCCAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTCCA 93
51 GGAGCAGGCCAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTCCA 100
94 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCGAAGAGCAGTA 143
101 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCGAAGAGCAGTA 150
144 CTGGGATCCTCTGCTGGGTACCTGCATGTCCCTGCAAAACCATTGCAACC 193
151 CTGGGATCCTCTGCTGGGTACCTGCATGTCCCTGCAAAACCATTGCAACC 200
194 ATCAGAGCCAGCGCACCTGTGCAGCCTCTGCAGGTCACTCAGCTGCCGC 243
201 ATCAGAGCCAGCGCACCTGTGCAGCCTCTGCAGGTCACTCAGCTGCCGC 250
244 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 293
251 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 300
294 TGCCTCCATCTGTGGACAGCACCCCTAACGAATGTGCATACTTCTGTGAGA 343
301 TGCCTCCATCTGTGGACAGCACCCCTAACGAATGTGCATACTTCTGTGAGA 350
344 ACAAGCTCAGGAGCCCAGTGAACCTCCACCAAGAGCTCAGGAGACAGCGG 393
351 ACAAGCTCAGGAGCCCAGTGAACCTCCACCAAGAGCTCAGGAGACAGCGG 400

FIG. 17

Human AGP3 receptor sequence

GTCGACCCACCGTCCGATCCTGACTAATGAGTGGCCTGGGCCGGAGCAGGGCAGGGTGGC
M S G L G R S R R R G G
CGGAGCCGTGACCGAGGAGGAGCGCTTCCACAGGGCCTGTGGACAGGGTGGCTATG
R S R V D Q E E R F P Q G L W T G V A M
AGATCCTGCCCGAAGAGCAGTACTGGATCCTCTGCTGGTACCTGCATGCTCTGCAAA
R S C P E E Q Y W D P L L G T C M S C K
ACCATTGCAACCATCAGAGCCAGCGCACCTGTGCAGCCTCTGCAGGTCACTCAGCTGC
T I C N H Q S Q R T C A A F C R S L S C
CGCAAGGAGCAAGGCAAGTTCTATGACCATCTCTGAGGGACTGCATCAGCTGTGCCTCC
R K E Q G K F Y D H L L R D C I S C A S
ATCTGTGGACAGCACCCCTAACAGCAATGTGCATACTCTGTGAGAACAGCTCAGGAGCCCA
I C G Q H P K Q C A Y F C E N K L R S P
GTGAACCTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACAATTCA
GAC V N L P P E L R R Q R S G E V E N N S D
AACTCGGGAAAGGTACCAAGGACTGGAGCACAGAGGCTCAGAACAGCAAGTCCAGCTCTCCCG
N S G R Y Q G L E H R G S E A S P A L P
GGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGCTCTGCCTG
G L K L S A D Q V A L V Y S T L G L C L
TGTGCCGTCCCTGCTGCTCCTGGTGGCGGTGGCCTGCTCCTCAAGATGAGGGGGGAT
C A V L C C F L V A V A C F L K M R G D
CCCTGCTCCCTGCCAGCCCCGCTCAAGGCCCCGCTAAAGTCCGGCAAGTCTCCAGGAT
P C S C Q P R S R P R Q S P A K S S Q D
CACCGCGATGGAAGCCGGCAGCCCTGTGAGCACATCCCCGAGCCAGTGGAGACCTGCAGC
H A M E A G S P V S T S P E P V E T C S
TTCTGCTTCCCTGAGTGCAGGGGCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCC
F C F P E C R A P T Q E S A V T P G T P
GACCCCACCTGTGCTGGAAGGTGGGGTGCACACCAGGACCACAGTCCTGCAGCCTTGC
D P T C A G R W G C H T R T T V L Q P C
CCACACATCCCAGACAGCGGCCCTGGCATTGTGTGCCTGCCAGGAGGGGGCCA
P H I P D S G L G I V C V P A Q E G G P
GGTGCATAATGGGGTCAGGGAGGGAAAGGAGGAGGGAGAGATGGAGAGGAGGGAG
G A
AGAGAAAGAGAGGTGGGGAGAGGGAGAGAGATATGAGGAGAGAGAGACAGAGGAGGCAG
AGAGGGAGAGAAACAGAGGAGACAGAGAGGGAGAGAGAGACAGAGGGAGAGAGACAGA
GAGGAAGAGAGGCAGAGAGGGAAAGAGGAGAGGAGAGGAAGGAAAGAGACAGGCAGAGAAGGAGA
GAGGCAGAGAGGGAGAGAGGCAGAGAGGGAGAGAGGAGAGGAGAGACAGAGAGGGAGAGGAG
GACAGAGAGAGATAGAGCAGGAGGTGGGGCACTCTGAGTCCCAGTCCAGTGCAGCTG
TAGGTGTCATCACCTAACACACAGTGAATAAGTCCCTGCTGCCTGCTCACAGCCC
CCGAGAGCCCCCTCCTCTGG

FIG. 18
AGP3 receptor protein structure

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMR

SCPEEQYWDPLLGTMSCKTICNHQSQRTCAAFCRSL I

SCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENK II

LRSPVNLPPPELRRQRSGEVENNSDNSGRYQGLEHRGSE stalk
ASPALPGLKLSADQVAVYS

TLGLCLCAVLCCFLVAVACFL TM

KMRGDPCSCQPRSRRQSPAKSSQDHAMEAGSPVSTSP IC
EPVETCSFCFPECRAPTQESAVTPGTPDTCAGRWGCHT
RTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

FIG. 19

Alignment of AGP3 receptor and TNFR1 extracellular domain

| 10 | 20 | 30 | 40 | 50 | 60 | |
|---|---------------------|----------------|-------|-----------------|----|-------|
| LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPPEEQYWDPLLGTTCM | SC | KTICNHQS-QR | | | | AGP3R |
| VLLELLVGIYPSGVIGLVPHLGDR | EKRD | SVCPQGKYIHPQNN | SIC | --C-TKCHKGTYLYN | | TNFR1 |
| 20 | 30 | 40 | 50 | 60 | 70 | |
| 70 | 80 | 90 | 100 | 110 | | |
| TCAAFCRSLSCRK-EQGKF-YDHLLRDC | ISCASICGQHPKQCAYFC | CENKLRSPVNLPPE | | | | AGP3R |
| DCPGPGQDTDCRECESGSFTASENH | LRHCLSC-SKCRKEMGQVE | ISSCTVDRDTVC | GGCRK | | | TNFR1 |
| 80 | 90 | 100 | 110 | 120 | | |

FIG. 20

Human AGP3 receptor mRNA tissue distribution

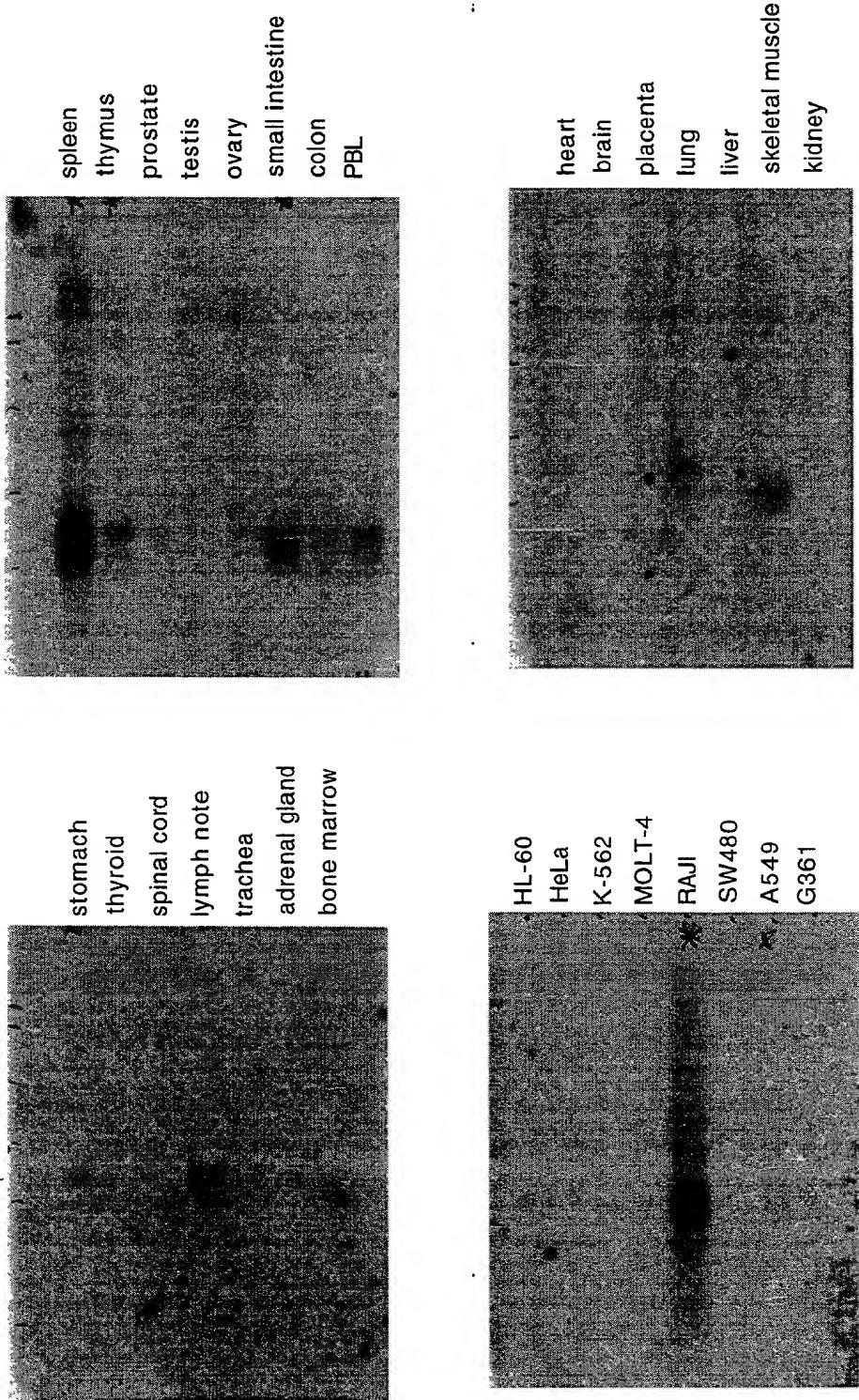


FIG 21

